Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure;

2) A printout of the web page describing the "EZ-Detect Rho Activation Kit" from Pierce Biotechnology;

3) A printout of the web page describing "Rhotekin-RBD Protein GST Beads" from Cytoskeleton, Inc.;

4) A printout of the web page describing "Rhotekin Rho Binding Domain, agarose" from Upstate Cell Signaling Solutions;

5) A copy of Reid et al., "Rhotekin, a New Putative Target for Rho Bearing Homology to a Serine/Threonine Kinase, PKN, and Rhophilin in the Rho-binding Domain", J. Biol. Chem. 271:13556-13560 (1996);

6) An associate power of attorney appointment.

IN THE SPECIFICATION:

(1) Please delete the paragraph beginning at line 28 on p. 18 and continuing to line 8 on p. 19 and replace with the following replacement paragraph:

Accordingly, four overlapping cDNA clones that together can be used to provide an assembled consensus sequence spanning the GRBP-2 cDNA were deposited in a public repository (American Type Culture Collection, Manassas, Virginia, USA) on June 27, 2001 and collectively been assigned accession no. PTA-3484. Clone 1 (designation grbp2-5r1) contains nucleotides 1 - 742 (numbering as in FIG. 3), clone 2 (designation grbp2-rt1) contains nucleotides 419 - 1360, clone 3 (grbp2-3f13) contains

nucleotides 724 - 2748, and clone 4 (grbp2-rt5) contains nucleotides 1314 - 3489, plus the poly-A tail. Any errors in sequence reported herein can be determined and corrected by sequencing nucleic acids propagated from the deposited clones using standard techniques.

(2) Please delete the paragraph on p. 20 starting at line 3 and ending at line 10 and replace with the following replacement paragraph:

For purposes herein, percent identity of two nucleic acid sequences is determined using the procedure of Tatiana *et al.*, "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250 (1999), which procedure is effectuated by the computer program BLAST 2 SEQUENCES, available online at the National Center for Biotechnology Information (NCBI) website.

(3) Please delete the paragraph on p. 53 starting at line 10 and ending at line 20 and replace with the following replacement paragraph:

In a first such embodiment, the invention provides an isolated nucleic acid comprising (i) the assembled consensus nucleotide sequence of the four overlapping cDNAs deposited at the ATCC on June 27, 2001 and collectively accorded accession no. PTA-3484, (ii) the nucleotide sequence of SEQ ID NO: 1, or (iii) the complement of (i) or (ii). The assembled consensus nucleotide sequence of the four overlapping nucleic acids of

the ATCC deposit has, and SEQ ID NO: 1 presents, the entire cDNA of human GRBP2, including the 5' untranslated (UT) region and 3' UT.

(4) Please delete the paragraph on p. 78 starting at line 6 and ending at line 14 and replace with the following replacement paragraph:

Bacterial cells can be rendered electrocompetent — that is, competent to take up exogenous DNA by electroporation — by various pre-pulse treatments; vectors are introduced by electroporation followed by subsequent outgrowth in selected media. An extensive series of protocols is provided online in Electroprotocols Online: Collection of Protocols for Gene Transfer (Bulletin #1029735, BioRad, Richmond, CA, USA).

(5) Please delete the paragraph on p. 81 starting at line 23 and ending at line 32 and replace with the following replacement paragraph:

For purposes herein, percent identity of two amino acid sequences is determined using the procedure of Tatiana *et al.*, "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250 (1999), which procedure is effectuated by the computer program BLAST 2 SEQUENCES, available online at the National Center for Biotechnology Information (NCBI) website.

(6) Please delete the paragraph starting at line 27 on p. 102 and ending at line 6 on p. 103 and replace with the following replacement paragraph:

In a first series of protein embodiments, the invention provides an isolated human GRBP2 polypeptide having an amino acid sequence encoded by the assembled consensus nucleotide sequence of the four overlapping cDNAs deposited at the ATCC on June 27, 2001 and collectively accorded accession no. PTA-3484, or the amino acid sequence in SEQ ID NO: 3, which are full length human GRBP2 proteins. When used as immunogens, the full length proteins of the present invention can be used, inter alia, to elicit antibodies that bind to a variety of epitopes of the several forms of human GRBP2 protein.

(7) Please delete the paragraph starting on p. 119 at line 10 and ending at line 18 and replace with the following replacement paragraph:

In a first series of antibody embodiments, the invention provides antibodies, both polyclonal and monoclonal, and fragments and derivatives thereof, that bind specifically to a polypeptide having an amino acid sequence encoded by the assembled consensus of the four cDNAs deposited in the ATCC on June 27, 2001 and collectively accorded accession no. PTA-3484, or that have the amino acid sequence in SEQ ID NO:3, which are full length human GRBP2 proteins.

(8) Please delete the paragraph starting on p. 129 at line 13 and ending at line 16 and replace with the following replacement paragraph:

The human GRBP2 cDNA was deposited at the American Type Culture Collection (ATCC) on June 27, 2001 as four overlapping cDNA fragments collectively accorded accession number PTA-3484.

(9) Please delete the paragraph starting at line 30 on p. 131 and continuing to line 2 on p. 132 and replace with the following replacement paragraph:

Motif searches using Pfam (Washington University, St. Louis, web site), SMART (European Molecular Biology Laboratory, Heidelberg, web site), and PROSITE pattern and profile databases (Expert Protein Analysis System (ExPASy) web site), identified several known domains shared with mouse Grbp1 and Grbp2.

(10) Please delete the paragraph starting at line 32 on p. 132 and continuing to line 4 on p. 133 and replace with the following replacement paragraph:

Transcription factor binding sites were identified using MOTIF, available at the GenomeNet web site (Bioinformatics Center, Institute for Chemical Research, Kyoto University), including a binding site for MZF1 (917-924 and 927-934 bp), for cap (cap signal for transcription initiation,